

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 19:42:15 (Search time 2002.99 Seconds
(without alignments) 6149.166 Million cell updates/sec

Title: US-09-597-771-11

Sequence: 1 aaagaatcctagagagagagaa.....gcataaaaaaaaaaaaaa 780

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_hlg: *
3: gb_in: *
4: gb_com: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_com: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vi: *
30: em_htg_hum: *
31: em_htg_in: *
32: em_htg_other: *
33: em_htgo_in: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	780	100.0	780	6	AX068851	Sequence
2	765	98.1	779	8	AF296084	Lycopersi
3	640.4	82.1	733	8	AB004824	Solanum t
4	396	50.8	632	8	AB004827	Solanum t
5	386.2	49.5	760	8	AF296086	Lycopersi
6	385.4	49.4	716	8	AB004823	Solanum t
7	349.6	44.8	925	8	AF323604	Solanum t
8	349.6	44.8	1288	8	AF266464	Manihot e
9	343.8	42.4	1124	8	NP001F5A2	Manihot e
10	330.8	42.4	713	8	AF296085	Lycopersi
11	328.4	42.1	726	8	AB004825	Solanum t
12	319.8	41.0	649	8	AF416338	Medicago
13	318.6	40.8	725	8	AF225297	Euphorbia
14	313.8	40.2	688	8	AB004826	Solanum t
15	309.8	39.7	810	8	AF296081	Solanum t
16	309.8	39.7	812	6	AX068853	Dianthus
17	307.6	39.4	741	8	MS01F4DMR	Sequence
18	305.4	39.2	722	8	OS4252135	M.sativa
19	302.6	38.8	715	8	AF296083	Oryza sat
20	300	38.5	480	8	SYE238624	Senecio v
21	298.6	38.3	676	8	AY063780	Arabidops
22	298.6	38.3	702	6	AX068855	Arabidops
23	298.6	38.3	702	8	AF296082	Arabidops
24	297.4	38.1	807	8	ZMRTR1F5A	Arabidops
25	292.4	37.5	822	8	AF094773	Oryza sat
26	288.8	37.0	676	8	AF372933	Arabidops
27	288.6	37.0	831	8	AF034943	Zea mays
28	286.6	36.7	765	8	AY039588	Arabidops
29	283.8	36.4	480	8	AY055789	Arabidops
30	283.8	36.4	702	8	NP001F5A1	N.plumbagin
31	282.2	36.2	477	8	AY060530	Arabidops
32	182.2	23.4	433	8	RIC225	Rice
33	165.4	21.2	2156	8	YSCANBI	S.cerevisia
34	165.4	21.2	2472	8	SCYJR047C	S.cerevisia
35	165.4	21.2	2538	8	SCHYPL	Yeast
36	165.4	21.2	42500	8	YSCGTGMS	S.cerevisia
37	163.8	21.0	745	8	YSCITF51B	S.cerevisia
38	162.2	20.8	167764	2	AP004303	Oryza sat
39	161	20.6	199551	2	AC006381	Plasmid
40	159.4	20.4	1053	3	AF109731	Spodopter
41	158.2	20.3	1050	3	AF109730	Spodopter
42	154	19.7	474	6	AX001142	Sequence
43	154	19.7	738	8	YSCIEF5A	S.cerevisia
44	154	19.7	1394	8	YSCITF51A	S.cerevisia
45	154	19.7	1923	8	SCHYPL2	Yeast

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	AX068851	Sequence 11 from Patent WO0102592.	AX068851	AX068851.1	GI:12578704		tomato.					

LYCOPERSICON ESCULENTUM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 780)
Thompson, J.E., Wang, T.W. and Lu, D.L.
Dna encoding a plant deoxyhypusine synthase, a plant eukaryotic initiation factor 5a, transgenic plants and a method for controlling senescence and programmed cell death in plants
Patent: WO 0102592-A 13 11-JAN-2001.
Senesco, Inc. (US)
Location/Qualifiers
1..780
/organism="Lycopersicon esculentum"

/db_xref="taxon:4081"
/note="elf-5A"
43..525
/note="unnamed protein product"

/codon_start=1
/protein_id="CAC27267.1"
/db_xref="GI:12578705"
/translation="MSDEHHFESKADAGASKTFPOAGTIRKNGYIVIKRPPCKVVE
VSTKRGHAKCHFYAIDIFNGKLEIDVPSHNCDDPHYRNPDYQILIDISEGCV
SLTESGNTKDLRLPDEMLKQVKGDFQEGKDLVYSVMSAMGEQINAVKDVGTKN"

BASE COUNT 253 a 141 c 171 g 215 t
ORIGIN

Query Match 100.0%; Score 780; DB 6; Length 780;
Best Local Similarity 100.0%; Pred. No. 1.3e-183;

Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaagaatcctagaagagaagaaggaatcctagaagagaagcaatgtcgaagaagacac 60
DB 1 AAGGAATCCTAGAGAGAGAAAGGAATCTAGAGAGAGAGCATGTGCGAAGAAACAC 60
QY 61 catcttgagtcgaagcagatgctgctgctcaaaacttcccaagcagctggaac 120
DB 61 CATTTGAGTCGAAGCAGATGCTGTGCTCAAAAACCTTCCACAGCAGCAGCTGGAAC 120
QY 121 atccgtgaagatggttaacatcgattcaaaagccgtccctcgaaggttgttgagctcc 180
DB 121 ATCCGTGAAGATGTTAATCGTTATCAAAAGCCGTCCCTGCAAGGTGTGTGAGGTCTCC 180
QY 181 acttcaaaactggaagacacgagcatgtcaatgtcactttgtgcaattgacatttc 240
DB 181 ACTTCAAAAACCTGGAAGACGAGCATGCTAAAGTCACTTTGTGGCAANTGACATTTTC 240
QY 241 aatggaagaagaactggaagatcgctccgtccctcccaaatgtgtgtgcaactgtt 300
DB 241 AATGGAAGAAGAAGTGAAGATATCGTCCGCTCCCAAAATGTGATGTGCGACATGTT 300
QY 301 aaccgtaccgaactacgaactgatatctctgaagaatggtttgttctcaacttctact 360
DB 301 AACCGTACCGACTATCAGCTGATGATCTCTGAGAGATGTTGTGCTCAGCTCTTACT 360
QY 361 gaaagtggaagacacacagatgactcaggttcccaagcagtaaaatctgtcgaagcag 420
DB 361 GAAAGTGGAACACCAAGGATGACTCAGGCTCCACCGATGAATCTGTGAAAGCAG 420
QY 421 gttaaagatgggttccagaagaagaagatctgtgtgtgtgttctgtcgtatggc 480
DB 421 GTTAAAGATGGGTTCCAGGAAGAAAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 481 gaagagcagatcaacgcggtcaagatgtgtgtccaaagaaatgaatgtcgtgacg 540
DB 481 GAAGACCAATTAACGCGGTTAAGGATGTGTGTCAAGAAATTAATGATGTGTGTGTGTGT 540
QY 541 ataatcagtcgaagaacttgaagacatcatatccataatgtgtgacttgaatcact 600
DB 541 ATAAATCAGTCGAAGCTTTAAAGACATATCATCTTAATGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 agatttaaacgtgttatttggcactgttcaaaaacaaagaagaagaactgctgtatag 660
DB 601 AGATTTAATCACTGTGTATTGTTCATGTCTAAACAAAGAAAGAAAGAAAGCTGTATAG 660
QY 661 ctgaagaagaatctgtgacttgaagcagacagctggaactgtgaaatctctc 720
DB 661 CTGAGAGAAAGATGTGGCTTTGAGCTTTGACAGCAGCAGTGTGAAATGTGAAATCTTAC 720
QY 721 ttttttttttgggtaaaataacgctcgtttaaagtgttggcaaaaaaataaaaaa 780
DB 721 TTTTGT 780

RESULT 2

AF296084 779 bp mRNA linear PLN 14-MAY-2001
LOCUS
DEFINITION Lycopersicon esculentum eukaryotic translation initiation factor
5A-2 mRNA, complete cds.
ACCESSION AF296084.1 GI:12407788
VERSION
KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE

AUTHORS
TITLE
JOURNAL
PUBMED
2 (bases 1 to 779)
Wang, T.-W., Lu, L., Wang, D., and Thompson, J.E.
Isolation and Characterization of Senescence-Induced cDNAs Encoding
Deoxyhypusine Synthase and Eukaryotic Translation Initiation Factor
5A from Tomato
J. Biol. Chem. 276 (20), 17541-17549 (2001)
11278418

FEATURES

Source

1..779
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
43..525
/note="elf-5A2"

CDS

/product="eukaryotic translation initiation factor 5A-2"
/protein_id="AF53648.1"
/db_xref="GI:12407789"
/translation="MSDEHHFESKADAGASKTFPOAGTIRKNGYIVIKRPPCKVVE
VSTKRGHAKCHFYAIDIFNGKLEIDVPSHNCDDPHYRNPDYQILIDISEGCV
SLTESGNTKDLRLPDEMLKQVKGDFQEGKDLVYSVMSAMGEQINAVKDVGTKN"

BASE COUNT 251 a 141 c 171 g 216 t
ORIGIN

Query Match 98.1%; Score 765; DB 8; Length 779;
Best Local Similarity 99.7%; Pred. No. 7.2e-180;

Matches 777; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 aaagaatcctagaagagaagaaggaatcctagaagagaagcaatgtcgaagaagacac 60
DB 1 AAGGAATCCTAGAGAGAGAAAGGAATCTAGAGAGAGAGCATGTGCGAAGAAACAC 60
QY 61 catcttgagtcgaagcagatgctgctcaaaacttcccaagcagctggaac 120
DB 61 CATTTGAGTCGAAGCAGATGCTGTGCTCAAAAACCTTCCACAGCAGCAGCTGGAAC 120
QY 121 atccgtgaagatggttaacatcgattcaaaagccgtccctcgaaggttgttgagctcc 180
DB 121 ATCCGTGAAGATGTTAATCGTTATCAAAAGCCGTCCCTGCAAGGTGTGTGAGGTCTCC 180
QY 181 acttcaaaactggaagacacgagcatgtcaatgtcacttttggaaatgaacttttc 240
DB 181 ACTTCAAAAACCTGGAAGACGAGCATGCTAAAGTCACTTTGTGGCAANTGACATTTTC 240
QY 241 aatggaagaagaactggaagatcgctccgtccctcccaaatgtgtgtgcaactgtt 300
DB 241 AATGGAAGAAGAAGTGAAGATATCGTCCGCTCCCAAAATGTGATGTGCGACATGTT 300
QY 301 aaccgtaccgaactacgaactgatatctctgaagaatggtttgtcgaacttctact 360
DB 301 AACCGTACCGACTATCAGCTGATGATCTCTGAAGATGTTGTGTCTACTTTTACT 360
QY 361 gaaagtggaagacacacagatgactcaggttcccaagcagtaaaatctgtcgaagcag 420
DB 361 GAAAGTGGAACACCAAGGATGACTCAGGCTCCACCGATGAATCTGTGAAAGCAG 420

D	b	361	GAAAGTGAACAACCAAGATGTCACCTCAGCGTTCCACCAGTGAATAAATCTGCTGAAGCAG	420
Oy		421	gttaagaatggttccaggaagaaggactcttgtagtcgtttacgtctgcagtggc	480
D	b	421	GTTAAGAATGGGTCCAGAGAAAGCATCTTGCTGTATGTCTGCAGATGGC	480
Oy		481	gaagaacagattaaacgcccttaagatcttgataccaagaattagtatgatcgacc	540
D	b	481	GAAAGCACATTAAACGCCCTTAAGATCTTGATCCAAGAAATTAGTATGTATGTGCAAC	540
Oy		541	-ataatcacctgccaaagcttaangaacattaatcatctcaatgtagtaccttgalatca	598
D	b	541	ATATATCACTCGCAAAGCTTAAACATTAATCACTCAAAAGTGTACTTGAATCA	600
Oy		599	ctgattataaacctgattatcttgacgttccaacaagaagaagaacgcgttat	658
D	b	601	CTGATTTATTAACCTGTTATTTGCACGTTCAAAAAGAAAGAAACGCTTAT	660
Oy		659	gctagaagaagatctgcttgcttgaccttgacgcacagctgaactatgtgaaattct	718
D	b	661	GGCTPAGAAAGATTTGGCTTTGACCTTTTACGACACAGTTAACATGTGAAATCT	720
Oy		719	acttttttttttggttaaatactgctgctttaagtttccaaaaaaaataaa	777
D	b	721	ACTTTTTTTTTTGGGTAAATACGTGCTCTTTAATGTTTGCAAAAAATAAAAAA	779
RESULT		3		
AB004824				
LOCUS				
DEFINITION			Solanum tuberosum mRNA for eukaryotic initiation factor 5A3,	
ACCESSION			complete cds.	
VERSION			AB004824.1 GI:2225880	
KEYWORDS			eukaryotic initiation factor 5A3.	
SOURCE			Solanum tuberosum (cultivar: Irish Cobbler) developing microtuber microtuber cDNA to mRNA.	
ORGANISM			Solanum tuberosum	
REFERENCE			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eucoyledons; core eucoicts;	
AUTHORS			Asteridae; euastrids I; Solanales; Solanaceae; Solanum.	
TITLE			1 (bases 1 to 733)	
JOURNAL			In,U.G.	
REFERENCE			Direct Submission	
AUTHORS			Submitted (13-JUN-1997) Jun Gyo In, Hokkaido University, Faculty of	
TITLE			Agriculture, Department of Botany; Kita 9 Nishi 9, Kita-Ku,	
JOURNAL			Sapporo, Hokkaido 060, Japan (E-mail: in642.hines.hokudai.ac.jp,	
REFERENCE			Tel:+81-11-706-2482, Fax:+81-11-706-2471)	
AUTHORS			2 (sites)	
TITLE			In,U.G., Fujino,K. and Kikuta,Y.	
JOURNAL			Nucleotide sequence of five cDNAs (Accession Nos.	
FEATURES			AB004823-AB004827) encoding eukaryotic translation initiation	
FACTORS			factor 5A (eif-5A) from potato (PG897.147)	
PLANT PHYSIOL.			Plant Physiol. 115, 864 (1997)	
LOCATION/QUALIFIERS			1.. 733	
ORGANISM			/organism="Solanum tuberosum"	
CULTIVAR			/cultivar="Irish Cobbler"	
DB_XREF			/db_xref="taxon:4113"	
TISSUE_TYPE			/tissue_type="microtuber"	
DEV_STAGE			/dev_stage="developing microtuber"	
GENE			/gene="eIF5A3"	
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CODON_START			/codon_start=1	
PRODUCT			/product="eukaryotic initiation factor 5A3"	
PROTEIN_ID			/protein_id="BAZ0877.1"	
DB_XREF			/db_xref="GI:2235881"	
TRANSLOCATION			/translocation="MSDEHHFESKADAGASKTYPOAQTIKKNCYIYIKOPCKVVE	
VSTSGTKGHAKCHFAVAIDFNPKADIEDVPSSHNCDDPVHNPFDYDLIDISEGFEV				
SLTSEGSNTKODLRLPDSEILSKQVDGEQKDVLVSVMASMBEQINALIKDIGTKNN				

BASE COUNT	232 a	142 c	166 g	193 t
ORIGIN				
Query Match	82.1%	Score 640.4;	DB 8;	Length 733;
Best Local Similarity	94.9%;	Pred. No. 7.1e-149;		
Matches 685; Conservative	0;	Mismatches 31;	Indels 6;	Gaps 2;

OY	11	agaagaagaagaagatctcgaagagaaagagatctgcagcaagaacaccatttgagt	70
Db	16	AGAAGGAAAGGGGAATCTTAGAAGACAGACATTCGACCAAGAACACCATTTTGAGT	75
OY	71	caaaggacaagatgctgtgacctcaaaaacttcccaagcaagctygaacacatccgtaaga	130
Db	76	CAAAGCAGATGTGCGTCTCAAAAACCTTAACCCACACAAGCTGGGAACCATCCGTAA	135
OY	131	atggttcacatcattatcaaaagggccfccccttgaaaaagttgttgaggtctcacattcaanaa	190
Db	136	ATGGTTCATATGTTATCAAAAGGCCGCTCCGTAAGGTTTGTAAGGTCTCCACTTCAAAAA	195
OY	191	ctggaaacaacacgycacatgctaaatgtgcaacttctgtgccaattgaacatllcaalygaaga	250
Db	196	CTGGAAAGCACGSGACATGCTTAATGTCACTTGTGGCAATGACATTTTCAATGGAAAGA	255
OY	251	aacgggaagatcatgttccgctccctcccaaatgtgatgtgcacatgtaaacocgtacacg	310
Db	256	AACGTGAGATATGTGTTCCATCTCCACAAATTTGAGCTGCACATGTCAACCGTRCCG	315
OY	311	actlacgctgatatcatctcgaagatggttttgtctcacttcttactgaagtgaagaa	370
Db	316	ACTATCAGCTGATGACATCTCTGAAGATGTTTTGTCTCCCTTCTTAAGTGAAGTGAA	375
OY	371	aacaccaagatgaacctgaagcttccccacgataagaaatctgtgaagcaagtttaaagatg	430
Db	376	ACACCAAGATGACCTCCGCTTCCCACGAGTAAGAGTCTGCTAAGACAGGTTTAACATG	435
OY	431	ggttcacgaagaagaagatctgtgtgtgtgtctgtatgtctlqcgatgpgcgaagacaga	490
Db	436	GGTTCCAGAGGAAGAAAGATCTGTGGTGTCTGTTATGTCTGCATGGGAGAACAGCAGA	495
OY	491	ttaagcgcttaagaagatggtgtgtagcaaaaatgtagttaatgtacatgagcaagat--aatcac	548
Db	496	TTAATGCCATTAAAGATATTGGTACCAAGATTAATGTTGTGCTGGCAGCATCTATAAATCAC	555
OY	549	tgcacaagctttaagaacatcatcatatccatlaigtlygtaclttgatalcatcatgattata	608
Db	556	TGCCAAACCTTAAGACATTAATTAACCTAATGAGGTACTTGAATATCACTAGATTATA	615
OY	609	aacgtgttatcttccactgttcaaaaacaaaagaagaacactgcgtgtatgagctcagaaga	668
Db	616	ATCTCTGTTATTTCACACTGTTGAAAACAAAGAAAGAAACTGCTGCTATAGGCTAAGAGA	675
OY	669	agatttgcttgagcttttgacagcacagttgaactatgtgaaatcttactctltttt	728
Db	676	AGTATGTGCTTTGAGCTTTTGACAGCACAGTTGAA---GTGAAATTCCTAATTATATT	731
OY	729	tt 730	
Db	732	AT 733	

RESULT	4	
AB004827	AB004827	632 bp mRNA linear PLN 05-FEB-1999
LOCUS	Solanum tuberosum mRNA for eukaryotic initiation factor 5A1,	
DEFINITION	complete cds.	
ACCESSION	AB004827	
VERSION	AB004827.1 GI:2225886	
KEYWORDS	eukaryotic initiation factor 5A1.	
SOURCE	Solanum tuberosum (cultivar:Irish Cobbler) developing microtuber	
	microtuber cDNA to mRNA.	
ORGANISM	Solanum tuberosum	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	

Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 632)

REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (13-JUN-1997) Jun Gyo In, Hokkaido University, Faculty of
Agriculture, Department of Botany, Kita 9 Nishi 9, Kita-ku,
Sapporo, Hokkaido 060, Japan (E-mail: inee2.hines.hokudai.ac.jp,
Tel:+81-11-706-2482, Fax:+81-11-706-2471)

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
2 (sites)
In,J.G., Fujino,K. and Kikuta,Y.
Nucleotide sequence of five cDNAs (Accession Nos.
AB004823-AB004827) encoding eukaryotic translation initiation
factor 5A (eIF-5A) from potato (PGR97-147)
Plant Physiol. 115, 864 (1997)
Location/Qualifiers

1..632
/organism="Solanum tuberosum"
/cultivar="Irish Cobbler"
/db_xref="taxon:4113"
/tissue_type="microtuber"
/dev_stage="developing microtuber"
43..525
/gene="eIF5A1"
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/protein_id="BA20880.1"
/db_xref="GI:225887"
/translation="MSDEEHFESKADAGASTYPOAGTIRKSGYIVIKGRPKYVE
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CDS
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43..525
/gene="eIF5A1"
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/product="eukaryotic initiation factor 5A1"
/protein_id="BA20880.1"
/db_xref="GI:225887"
/translation="MSDEEHFESKADAGASTYPOAGTIRKSGYIVIKGRPKYVE
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SLTENGNFTDRLRPTDALLNQVKGFEESKDLVLSVMSAMEEDICAVKDIGRTS
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BASE COUNT 185 a 121 c 147 g 179 t
ORIGIN

Query Match 50.8%; Score 396; DB 8; Length 632;
Best Local Similarity 82.7%; Pred. No. 4.3e-88;

Matches 453; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 2 aagaatcctagaagagaagaaggaatcctagaagagaagcatgttcgacgaagaacac 61
DB 2 aagaaag 61
QY 62 attctgaagcaagagcagatgtgtgtcctcaaaaacttccacagcagactggaacca 121
DB 62 attttgagtcCAAGAGCTGATGCTGCTCAAAACCTTACCTCAACAGCTGCTACTA 121
QY 122 tccgtaagaagaatgttaactgtttcaaaagccgctccgtaagaaggtttttgaggtctca 181
DB 122 ttggcgaagagtggtttatgtatgtatcaaaagcagaccttgcAAGGTTGAGGTCCTCA 181
QY 182 ctctcaaaaacttgaagaacacgagacatgtcaaatgttcacttgtgcaattgacattcca 241
DB 182 ctctcaaaaacttgaagaacacgagacatgtcaaatgttcacttgtgcaattgacattcca 241
QY 242 attggaagaagaactggaagaatgttcgctccctcccaaatgttgaatgagcacaatgttta 301
DB 242 attggaagaagaactggaagaatgttcttcttccatcccaaatgttgaatgagcacaatgttta 301
QY 302 accgtacacgactacatcgtatgtatctcgaagaatgttcttgcacttcttactg 361
DB 302 accgtacacgactacatcgtatgtatctcgaagaatgttcttgcacttcttactg 361
QY 362 aaagtgtgaagaacacgaagatgactcaggtctccacccgtaagaatctgcctgagacag 421
DB 362 aaagtgtgaagaacacgaagatgactcaggtctccacccgtaagaatctgcctgagacag 421
QY 422 tcaaatgtggttccaggaagaagagatcttgtgtgtctgttattgtctgcagatggagc 481
DB 422 ttaaaagtgagatttgaggaagaagaagatctgttctgtctgtgagatgtctgcaaatggagc 481

QY 482 aagacacagattaaagccgtaagaagatgtgtaccagaagaattatgtatcatgagcaga 541
DB 482 aagacacagattctgtctgttgAAGSACATTTGTCACAGACTAGTtGCCCTCATTTCTGCA 541

QY 542 taactact 549
DB 542 GCATTAAT 549

RESULT 5

AF296086 760 bp mRNA linear PLN 14-MAY-2001
LOCUS Lycopersicon esculentum eukaryotic translation initiation factor
DEFINITION 5A-4 mRNA, complete cds.
ACCESSION AF296086
VERSION AF296086.1 GI:12407792

KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 760)

REFERENCE
AUTHORS
TITLE
Wang,T.-W., Lu,L., Wang,D. and Thompson,J.E.
Isolation and Characterization of Senescence-Induced cDNAs Encoding
Deoxyhypusine Synthase and Eucaryotic Translation Initiation Factor
5A from Tomato
J. Biol. Chem. 276 (20), 17541-17549 (2001)
11278418

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (16-AUG-2000) Biology, University of Waterloo, Waterloo,
ON N2L 3G1, Canada
Location/Qualifiers

1..760
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/db_xref="taxon:4081"
55..537
/note="eIF-5A4"
/codon_start=1
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/protein_id="AA653650.1"
/db_xref="GI:12407793"
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VSTSKTGHAKCHVAIDIFNKKLEIVSSHNCVPHVNRDYLQIDISDGFV
SLTENGNFTDRLRPTDALLNQVKGFEESKDLVLSVMSAMEEDICAVKDIGRTS
"

CDS
/note="eIF-5A4"
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/db_xref="GI:12407793"
/translation="MSDEEHFESKADAGASTYPOAGTIRKSGYIVIKGRPKYVE
VSTSKTGHAKCHVAIDIFNKKLEIVSSHNCVPHVNRDYLQIDISDGFV
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BASE COUNT 235 a 141 c 159 g 225 t
ORIGIN

Query Match 49.5%; Score 386.2; DB 8; Length 760;
Best Local Similarity 84.0%; Pred. No. 1.2e-85;

Matches 436; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 31 agagagaagaagatgtcgagacgaagaacacatttgaatcgaagagcagatgtcgtgccc 90
DB 43 aagagatttggcattatgtcgaatgaagaacacatttgaatcgaagagcagatgtcgtgccc 102
QY 91 tcaaaaacttccacagcagacgtggaacatccgttaagaatgtttacatgttatacaaa 150
DB 103 tcaaaaacttccacagcagacgtggaacatccgttaagaatgtttatgtatgtatcaaa 162
QY 151 ggcgcgtccctgcaaggtgttctgaggtccacactcaaaaactggaagaacacagcagacatgct 210
DB 163 ggcgaacatttgcgaaggtgttctgaggtccacactcaaaaactggaagaacacagcagacatgca 222
QY 211 aaatgtcacttgtgtgcaatgtgacatttcaatgtgaagaagaactgtgaagatctcgtccg 270
DB 223 aaatgtcacttgtgtgcaatgtgacatttcaatgtgaagaagaactgtgaagatctcgtccg 282

Best Local Similarity	85.0%	Pred. No. 1	9e-85:	
Matches	431	Conservative	0	Mismatches 76; Indels 0; Gaps 0
QY	43	atgtcgacgaagaacacacatttgaagcaaaagcagatcgtgtgctccaaacttcc	102	
Db	57	ATGCTGATGAAGAAGACACCATTTTGAGTCCAAAGCTGATGCTGTGCTCCACAAACTTAC	116	
QY	103	ccacgcaagctcgggaacccctcgttaaatggttatacgtttataccaagcgccgtcgc	162	
Db	117	CCTCACCAAGCTGGTACTCTATTCGCAAGATGGTTATATAGTATATCAAAAGCAGACCTTGC	176	
QY	163	aaggttggtgaagtcctccactccaaaacctggaaacacaggaacatgctaatgctac	222	
Db	177	AAGGTTGTTGAGGTCTCCACTTCCAAAATGCGCAGACACGACATGCCAAAATGTCACTTT	236	
QY	223	gtggcaattgacatttccaaatggaaagaaacctgaaagatatcgttccgtcccccacat	282	
Db	237	GTGGCAATCGACATTTTCAATGGAAAAGAGCTTGAAGATATTGTTCCCTCATCCCAAT	296	
QY	283	tgtgtgtggcaacatgtaaaccttcacgacttcacgttcatgtattgatatcctgaagatgt	342	
Db	297	TGTGATGTGCCACATGTCAATGTACTGTCTATCACTGATTTGACATCTCTAAGATGGT	356	
QY	343	ttgtctcactcttactgaagctggaacacacaaagatgacctcaagcttccaccgat	402	
Db	357	TTTGTTGTCCTCTTACTGAAAATGGAAAACACCAAGAATGACCTCAGATTTCCACCGAT	416	
QY	403	ggaatctgctgaagcaggttaagaatggttccaggaagaaagatctgtgtgtct	462	
Db	417	GACGCCCTGTTTAAACAGGTTTAAAGTGTGATTGGAGGAAGCAAGCATCTGTTGTCT	476	
QY	463	gtatgctctcgatggcggaagacagatlaacgcgttaagaatggttgatccagaat	522	
Db	477	GTGATGCTGTGCAATGGGTGAAGACAGATCTGTGCTGTGAAGACATTTGTGAACCAAGAC	536	
QY	523	tagtaatgcatgycagcataatcact	549	
Db	537	TAGTTGCGCTCATCTCTGCAGCATAAAT	563	
RESULT	7			
AF323604				
LOCUS	AF323604	925 bp	mRNA	linear
DEFINITION	Manihot esculenta initiation factor eIF5-A mRNA, complete cds.			
ACCESSION	AF323604			
VERSION	AF323604.1	GI:13094962		
KEYWORDS				
SOURCE	CASSAVA.			
ORGANISM	Manihot esculenta			
REFERENCE	Enkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae: eucosids I; Malpighiales; Euphorbiaceae; Manihot.			
AUTHORS	1 (bases 1 to 925)			
TITLE	Reilly,K., Winter,M., Han,Y. and Beeching,J.			
JOURNAL	Manihot esculenta translation initiation factor eIF5-A			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 925)			
TITLE	Reilly,K., Winter,M., Han,Y. and Beeching,J.			
JOURNAL	Direct Submission			
FEATURES	Submitted (22-NOV-2000) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AY, UK			
SOURCE	Location/Qualifiers			
	1..925			
	/organism="Manihot esculenta"			
	/db_xref="taxon:3983"			
	51..923			
CDS	/note="eukaryotic translation initiation factor; formerly eIF4D; post-translationally modified to contain hypusine"			
	/codon_start=1			
	/transl_except="(pos:204..206,aa:OTHER)			
	/product="initiation factor eIF5-A"			
	/protein_id="AAK12100.1"			

misc_feature 201..221 /note="GKHGXAK; Region: conserved hypusination motif"
BASE COUNT 305 a 161 c 203 g 256 t
ORIGIN

Query Match 44.8%; Score 349.6; DB 8; Length 925;
Best Local Similarity 79.8%; Pred. No. 1.5e-76;
Matches 412; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 31 agagagaagaagcagtcgagcagaagaacaacatttgatgcaagcagatgctgctc 90
DB 39 AGAAAAACGCTATGTCGAGCAGAGACACCACTTCGAGTCCAGACGCGATCCTGGAGCC 98
QY 91 tcaaaacttcccaagaagaagctggaaccatcgtaagaatggttatactgtaaa 150
DB 99 TCCAAAGACCTTCCACACAGCTGGTACCATTCGCAAGAAAGGCTTACATCTTAATCAAG 158
QY 151 ggcgcctccgcaaggtgttgagtcctcaactcaaaaactggaacaacgagacatgct 210
DB 159 AATGTCCTCGCAGAGGTTATGGAGTTTCAACATCAAAAGACGGAAACATGTCATGCT 218
QY 211 aaatgtaacttggcgaattgaacatttcaatggaagaacaactggaagatgcttcg 270
DB 219 AAGTGCATTGTTGTTGGAATGATATATTCATGGAAGAAAAAATCGAATATTTTCT 278
QY 271 tctcccaaatgtgtatgttcacacatgttaaccgtacagactacagtgatgatalc 330
DB 279 TCATCCACACATGTGATGTTCTCTCATGTTAACCTGACTGATTATACAGTTATATAC 338
QY 331 tctgaagaatggtttgtctcactcttactgaagtgaagaacaacaagaatgactcag 390
DB 339 TCGAAGATGTTGTTGATGTTGATGTTGAACTGAAACACCAAGACGATCTCAG 398
QY 391 ctcccaacgagatgaataatgctgaagcaggttaagaatgggttccagaagaagaagat 450
DB 399 CTTCCACACCATGATAAATGCTCAAGCAGATTAAAGATGGTTGCTGAAGGAGAGAC 458
QY 451 ctgtggtgtctgtatgtctgcagatggcggaagacagatlaaacgcgttaagaatgct 510
DB 459 CTGCTAGTAGGCTCATGTTGTCATATGGAGAGAGAGAGGATATGTTCCCTTAAGCAT 518
QY 511 gtiaccaagaatagttatgtcatgagcagataatc 546
DB 519 GGTCCTAAAAATTAAAGATGATGCTATAGCATTTAGC 554

RESULT 8
AF266464 1288 bp mRNA linear PLN 24-MAY-2001
LOCUS AF266464
DEFINITION Manihot esculenta translation initiation factor 5A mRNA, complete cds.
ACCESSION AF266464
VERSION AF266464.1 GI:14193248
KEYWORDS
SOURCE .
ORGANISM cassava.
Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Euphorbiales; Manihot.
REFERENCE
AUTHORS Reilly,K., Winter,M.J., Han,Y., Tohme,J. and Beeching,J.R.
TITLE Cassava translation initiation factor 5A (elf-5A)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1288)
AUTHORS Reilly,K., Winter,M.J., Han,Y., Tohme,J. and Beeching,J.R.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-2000) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AT, UK

FEATURES
source Location/Qualifiers
1..1288
/organism="Manihot esculenta"
/db_xref="taxon:3983"
CDS
71..553
/codon_start=1
/product="translation initiation factor 5A"
/protein_id="AAK55848.1"
/db_xref="GI:14193249"
/translation="MSDEHHFESKADNAGASKTPPOAGTIRKNGYIVIKNPKYME
VSTSKTGHGAKCHVEGIDIFNGKLEIDYVSSHNCVPHNRPDIOLDISDEGCV
SLTETGNTKDLRLPTDENLLSQIKDGFAGKDLVVSVMAMGEERICSCLKDIGPN"

BASE COUNT 428 a 222 c 293 g 345 t
ORIGIN

Query Match 44.8%; Score 349.6; DB 8; Length 1288;
Best Local Similarity 79.8%; Pred. No. 1.5e-76;
Matches 412; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 31 agagagaagaagcagtcgagcagaagaacaccattttagcacaagaagaatgctgctc 90
DB 59 AGAAAAACGCTATGTCGAGCAGAGAACCACTTCGAGTCCAAAGGCGATGCTGAGCC 118
QY 91 tcaaaacttcccaagaagaagctggaaccatcgtaagaatggttatactgtaaa 150
DB 119 TCCAAAGACCTTCCACACAGCTGGTACCATTCGCAAGAAATGGCTTACATCTTAATCAAG 178
QY 151 ggcgcctccgcaaggtgttgagtcctcaactcaaaaactggaacaacgagacatgct 210
DB 179 AATGTCCTCGCAGAGGTTATGGAGTTTCAACATCAAAAGACGGAAACATGTCATGCT 238
QY 211 aaatgtaacttggcgaattgaacatttcaatggaagaacaactggaagatgcttcg 270
DB 229 AAGTGCATTGTTGTTGGAATGATATATTCATGGAAGAAAAAATCGAATATTTTCT 278
QY 271 tctcccaaatgtgtatgttcacacatgttaaccgtacagactacagtgatgatalc 330
DB 299 TCATCCACACATGTGATGTTCTCTCATGTTAACCTGACTGATTATACAGTTATATAC 358
QY 331 tctgaagaatggtttgtctcactcttactgaagtgaagaacaacaagaatgactcag 390
DB 359 TCTGAAGATGTTGTTGATGTTCTCTCATGTTAACTGAAACACCAAGAGATCTTAGG 418
QY 391 ctcccaacgagatgaataatgctgaagcaggttaagaatgggttccagaagaagaagat 450
DB 419 CTTCCACACGATGATAAATCTGCTCAGCCAGATTAAAGATGGTTGCTGAAGGAGAGAC 478
QY 451 ctgtggtgtctgtatgtctgcagatggcggaagacagatlaaacgcgttaagaatgct 510
DB 479 CTGCTAGTAGGCTCATGTTGTCATATGGAGAGAGAGGATATGTTCCCTTAAGCAT 538
QY 511 gtiaccaagaatagttatgtcatgagcagataatc 546
DB 539 GGTCCTAAAAATTAAAGATGATGCTATAGCATTTAGC 574

RESULT 9
NP01552 1224 bp mRNA linear PLN 13-FEB-1992
LOCUS NP01552
DEFINITION N-plumbaginifolia mRNA NeIF-5A2 for Initiation factor 5A(2).
ACCESSION X63542
VERSION X63542.1 GI:19701
KEYWORDS hypusine-containing protein; initiation factor; translation initiation factor.
SOURCE curled-leaved tobacco.
ORGANISM Nicotiana plumbaginifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Chamot,D.D.

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
Direct Submission	Submitted (13-DEC-1991)	D. Chamrot, Institute of Plant Physiology, University of Berne, Altenbergrain 21, CH- 3013 Berne, SWITZERLAND	2 (bases 1 to 1224)	Chamrot,D. and Kuhlmeier,C.	Differential expression of genes encoding the hypusine-containing translation initiation factor, eIF-5A, in tobacco	Nucleic Acids Res. 20 (4), 665-669 (1992)	92178957	See also X63541-3.
Location/Qualifiers	1..1224							
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/tissue_type="leaf"								
<1..38								
39..518								
/gene="NeIF-5A2"								
39..518								
/gene="NeIF-5A2"								
/codon_start=1								
/product="eukaryotic initiation factor 5A (2)"								
/protein_id="CAA5104.1"								
/db_xref="GI:19702"								
/db_xref="SWISS-PROT:P24922"								
/translation="MSDEEHOFESKADAGSKYPOQAGIRKNNGHIVIRGCKEYVEVSRSGKGGHAKCHPAIDIFFGKIEDIVPSRHNCDFVHNRITDQLDIDISDFVSLTLENSTKDDSLPTDDNLLTQIKDGFAGKDLVVSVMANGEGICALKDIGPK"								
519..>1224								
345 a	261 c	229 g	389 t					
BASE COUNT								
ORIGIN								

Query Match	44.1%	Score 343.8	DB 8	Length 1224
Best Local Similarity	79.5%	Pred. No. 4,3e-75		
Matches 419	Conservative 0	Mismatches 107	Indels 1	Gaps 1
QY 43 atgcgcagcgaaggaaccactcttgcagcaaggcaagtgctgtgctcaaaacttc	102			
Db 39 ATGTGGAACGAGGAGACCACTTTTATGTCAAAGGCCGATGCGGTGATCTTAACCTTAC	98			
QY 103 ccacagcaagcttgaaccatccgttaagatgtgtatcatcgtatcaaaagcgctccctgc	162			
Db 99 CCTCAACAAAGTGGTATACATCCGTAAAGACGGTCAATCGTCATCAACAAAGGCCGTCCGCG	158			
QY 163 aagtttgttgggtctccactctcaaaacttgaaaaacaggaactgtctaattgcacttt	222			
Db 159 AAGTGTGGGAAGTCTCTACATCCAAAACCGAAAGCACGGTCAATGCAAAATGTCTATTTT	218			
QY 223 gtggcaattgacatttccaatgtaagaagaacttgaagatatcgtctcgtctccacaat	282			
Db 219 GTGCGTATGTGACATCTTCACATGGAAGAAGCTTTAAGATATGTTTCCCTCTTCACACAT	278			
QY 283 tctgaatgtgcacacatgttaaccgtaccgaactacagtgtatgtatctctgaagaatgt	342			
Db 279 TGTATGTGCCCCACGTTAATCGTACAGATATATACAGCTTATGTGACATTTCTGAAGATGGA	338			
QY 343 ttgtccactcttacttgaagtgtgaacaaccaaagatgacctcaggtctccacgat	402			
Db 339 TTTTGTGATGTGCTCACTGTGAATATGTATACCCCAAGATGACCTTAGGCTTCTCAATGAT	398			
QY 403 gaaatctcgtcgaagcaggttaagaatgtgttccaagaaagaaagatcttgtgtct	462			
Db 399 GATTAACCTCTTACACAGATCAAGATGAAGATGGGTTTGTCTAAGGAAAAGACCTTGTGTCT	458			
QY 463 gttatcgtcgaatgggcgaagcagaattaaagccgttaagatgtgtgtgaagaagat	522			
Db 459 GTCATGTCAAGCCAAAGGGTGAAGACCAATTTGTGTCCCTGAAAGATATTTGGTCCCAAGTA	517			
QY 523 tagttatgtcatgtgcagcataatcactcgtccaaagctttaagacatla	569			
Db 518 AATCTCTTGAATGGAGATGTGCTGATGCGAAGCTTTTACACTTA	564			

LOCUS	AF296085	713 bp	linear	PLN 14-MAY-2001
DEFINITION	Lycopersicon esculentum eukaryotic translation initiation factor			
ACCESSION	AF296085			
VERSION	AF296085.1 GI:12407790			
KEYWORDS	. tomato.			
SOURCE	Lycopersicon esculentum			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Solanales; Solanaceae; Solanum;			
REFERENCE	1 (bases 1 to 713)			
AUTHORS	Wang,T.-W., Lu,L., Wang,D. and Thompson,J.E.			
TITLE	Isolation and Characterization of Senescence-Induced cDNAs Encoding Deoxyhypusine Synthase and Eukaryotic Translation Initiation Factor 5A from Tomato			
JOURNAL	J. Biol. Chem. 276 (20), 17541-17549 (2001)			
PIUMED	11278418			
REFERENCE	2 (bases 1 to 713)			
AUTHORS	Wang,T.-W., Wang,D., Lu,L. and Thompson,J.E.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-AUG-2000) Biology, University of Waterloo, Waterloo, ON N2L 3G1, Canada			
FEATURES	Location/Qualifiers			
Source	1..713			
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CDS	52..531			
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	/protein_id="AA033649.1"			
	/db_xref="gi:12407791"			
	/translation="MSDEHFEESKADAGASKYTPQOAGTIRKNGYIVIGRPCKVVEVSTKGTGHHGAKHFVAIDIFETGKEDYIPSSHNDVPHVNTDTOLDISDGFVSLINDNGTKNDLPLPNDENLSLKKGFAEGRKLVVYSMSAMEBDINALKDIGPR"			
BASE COUNT	195 a 135 c 155 g 228 t			
ORIGIN				
Query Match	42.4%; Score 330.8; DB 8; Length 713;			
Best Local Similarity	80.8%; Pred. No. 7.2e-72;			
Matches	386; Conservative 0; Mismatches 92; Indels 0; Gaps 0;			
OY	42	catgtcgaagaagaacacatttgagtcagaagcagatgctgtgtccccaacttt	101	
DB	51	CATGTCGACGAGGAGCATCAATTGAGCTTAAGCGTATCCGGAGCATCAAAAACCTTA	110	
OY	102	cccaagaagaactgtgaacacatccgtaagaatggttaactgcttcaaaagccgtccctg	161	
DB	111	CCCTCAACAGCTGGTACTATTTCGTAAAGCGTTATVCGTCATCAAAAGCCGTCATG	170	
OY	162	caaggttgttgaggtctccacttcaaaaactcggaaacaacagagacatgtctaaatgctact	221	
DB	171	CAAGGTGTGGAAGTCTCTACATCCAAAACGTGGCAGACGCGTACGCCAATATGTCATT	230	
OY	222	tgtggcaattgacatttcaatgtgaagaagaactgtgaagatacglttccgtccccaaca	281	
DB	231	CGTTGCTATTGACATCTTCACTCGGGAAMAACCTTGAGATATTGCGCCCTCTCACACAA	290	
OY	282	tttgatattgcaaatgttaacggtaccgactatcagttgattgatattcttgaagaatgg	341	
DB	291	TTTGATATTGCCCCATGTTAATTCGACAGATTATTCAGCTTATGACATCTCTGAAGATGG	350	
OY	342	tttttccacttctactgaagtgtgaacaacacgaagatgaactcaggtctccaccga	401	
DB	351	ATTGTGTAGTCTGCTACTAGCAATAGGTAAACACCAAGATATCACTCAGGCTTCTACTGA	410	
OY	402	tgaaatctgtcgaagcaggttaagaatggtgtccagaagaagaagatcttgtgttc	461	


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Db 411 TGAATATCGCTTTCACATGATCAAGACGGGTTTCCAGAGGTAAAGACCTCGTGTCTC 470
|||
Qy 462 tgtatgtcgcgatgagcgaagacagatlaacgcccgttaaggatgtgtgtaaccag 519
|||||
Db 471 TGTATGTCAGCTATGAGGAGGAGAACAGATTAAATGCTTTGAAGGATATTGGCCCCAAG 528
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RESULT 11
AB004825 726 bp mRNA linear PLN 05-FEB-1999
LOCUS Solanum tuberosum mRNA for eukaryotic initiation factor 5A4,
DEFINITION complete cds.
ACCESSION AB004825
VERSION AB004825.1 GI:2225882
KEYWORDS eukaryotic initiation factor 5A4,
SOURCE Solanum tuberosum (cultivar: Irish Cobbler) developing microtuber
microtuber cDNA to mRNA.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
In J.G.
REFERENCE 1 (bases 1 to 726)
AUTHORS Direct Submission
JOURNAL Submitted (13-JUN-1997) Jun Gyo In, Hokkaido University, Faculty of
Agriculture, Department of Botany; Kita 9 Nishi 9, Kita-ku,
Sapporo, Hokkaido 060, Japan (E-mail: in@a2.hines.hokudai.ac.jp,
Tel:+81-11-706-2482, Fax:+81-11-706-2471)
2 (sites)
REFERENCE In J.G., Fujino, K. and Kikuta, Y.
AUTHORS Nucleotide sequence of five cDNAs (Accession Nos.
JOURNAL AB004823-AB004827) encoding eukaryotic translation initiation
factor 5A (eif-5a) from potato (PGR97-147)
Plant Physiol. 115, 864 (1997)
FEATURES
source location/Qualifiers
1..726
/organism="Solanum tuberosum"
/cultivar="Irish Cobbler"
/db_xref="taxon:4113"
/tissue_type="microtuber"
/dev_stage="developing microtuber"
44..523
/gene="eif5A4"
44..523
/cds
/gene="eif5A4"
/codon_start=1
/product="eukaryotic initiation factor 5A4"
/protein_id="AAA20878.1"
/db_xref="GI:2225883"
/translation="MSDEHGFESKADAGASKTYPQAGTIRKSGYVIKRPCKVE
VSTSKTGHGAKCHFAVIDFTGKLEIDIVPSHNCDDVPHNRDYLIDISDGFV
SLTDNGSTMDKLPDLSLQIKDGFAGKDLVVSVMAMGEQINALDKIGPK"

BASE COUNT 185 a 137 c 162 g 242 t

Query Match 42.1%; Score 328.4; DB 8; Length 726;
Best Local Similarity 80.1%; Pred. No. 2.8e-71;
Matches 386; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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Qy 222 tgtgcaattgacatttcaatggaagaactggaagatalcgttcgtccctccacaa 281
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Qy 282 ttgtgatgtgccacatgtaaccgtaccactacagctgattgabatcctcgaagatg 341
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Db 283 TTGTGATGTGCCCATGTTTAAATCGACAGATPATCAGCTTATTGACATCTCGAAGATGG 342
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Qy 342 ttgtgtcactctctacggaagtggaacacacaaagatgacctcagctccacaga 401
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Db 343 ATTTGTGAGTCTCTCCTCACATGACATGTAAACACCAAGATGACCTTGCTTACCGA 402
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Qy 402 tgaatactctgtaagcaggttaagatggttcaggaaggaagatctgtgtgtc 461
|||||
Db 403 TGAATGCTGCTTTCACACAGATCAAGATGGGTTTGCTGAGGGTAAGACCTGTGTGTC 462
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Qy 462 tgtatgtcgcgatgagcgaagacagatlaacgcccgttaaggatgtgtgtaaccagaa 521
|||||
Db 463 TGTATGTCAGCTATGAGGAGTGAAGACAGATTATGCCCTGAAGATATTGGCCCCAAGTA 522
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Qy 522 tc 523
Db 523 AT 524

RESULT 12
AF416338 649 bp mRNA linear PLN 03-OCT-2001
LOCUS Medicago sativa eukaryotic translation initiation factor 5A-2 mRNA,
DEFINITION complete cds.
ACCESSION AF416338
VERSION AF416338.1 GI:15866586
KEYWORDS Medicago sativa.
SOURCE Medicago sativa.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliae;
Medicago.
REFERENCE 1 (bases 1 to 649)
AUTHORS Alfalfa translation initiation factor 5A-2 from salt tolerant
JOURNAL winicov, I.
TITLE unpublished
JOURNAL 2 (bases 1 to 649)
REFERENCE winicov, I.
AUTHORS Direct Submission
JOURNAL Submitted (31-AUG-2001) Plant Biology, Arizona State University,
Main Campus, PO Box 871601, Tempe, AZ 85287-1601, USA
FEATURES
source location/Qualifiers
1..649
/organism="Medicago sativa"
/strain="Regen S"
/db_xref="taxon:3879"
/tissue_type="callus"
/notes="salt tolerant cell line; grown continuously in 171
mM NaCl"
52..531
/codon_start=1
/product="eukaryotic translation initiation factor 5A-2"
/protein_id="AAL10404.1"
/db_xref="GI:1386587"
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VSTSKTGHGAKCHFAVIDFTGKLEIDIVPSHNCDDVPHNRDYLIDISDGFV
SLTDNGSTMDKLPDLSLQIKDGFADGKDLVVSVMAMGEQICALDKIGPK"

BASE COUNT 197 a 114 c 140 g 198 t

Query Match 41.0%; Score 319.8; DB 8; Length 649;
Best Local Similarity 78.2%; Pred. No. 3.9e-69;

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[illegible]

FEATURES	source
LOCUS	AF225297 725 bp mRNA linear PLN 26-JAN-2000
DEFINITION	Euphorbia esula translation initiation factor 5A mRNA, partial cds.
ACCESSION	AF225297
VERSION	AF225297.1 GI:6752916
KEYWORDS	.
SOURCE	leafy spurge.
ORGANISM	Euphorbia esula
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Malpighiales; Euphorbiaceae; Euphorbia.
AUTHORS	1 (bases 1 to 725)
TITLE	Anderson, J.V. and Horvath, D.P.
JOURNAL	Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge)
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 725)
TITLE	Anderson, J.V. and Horvath, D.P.
JOURNAL	Direct Submission
FEATURES	Submitted (14-JAN-2000) Plant Science, USDA/ARS, 1605 Albrecht Blvd., Fargo, ND 58105, USA
source	Location/Qualifiers
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	/clone="3"
	/tissue_type="3-day induced (defoliated) underground
	adventitious buds"
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	/codon_start=1
	/product="translation initiation factor 5A"
	/protein_id="AAP27938.1"
	/db_xref="GI:6752917"

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	POLYA_site	472 .725
	BASE COUNT	204 a 137 c 168 g 216 t
	ORIGIN	708
Query Match	40.8%; Score 318.6; DB 8; Length 725;	
Best Local Similarity	80.0%; Pred. No. 7.8e-69;	
Matches 375; Conservative	0; Mismatches 94; Indels 0; Gaps 0;	
OY	53	aagaaccattttagtcaaaagcagatgtctgttcctcaaaaactttccacagcaag 112
DB	2	ACGAGAGACCACCTTCAGGCTTAAGCGCCGACGCCGGTGCTTCAAAAGACTTACCTCAGCAAG 61
OY	113	cggagaccatccgtaagatatgttatcatcgatatcaaaaggcccgcgaagattgttg 172
DB	62	CTGGATCACCATCCGTAAAAACGGTTTCATTCGTATCATCAAGAACCCGCTCTTGCAAGGTTGTTG 121
OY	173	aggctccactccaanaacctggnaaacacagacatcgtcaaatgtlcatcttgygcaatg 232
DB	122	AGGTCTCAACATCCAAAGACTGGAAAGCAGCGGCATGSCAANAATGTCATTGTTGGAATTG 181
OY	233	acaatttcaaayggaaagaactygaagataatcgttcgtccotccccaaatgtgatgtgc 292
DB	182	AATATCTTCAAATGGAAAGAAGCTTGAAGATATCGTTCCTTCTCCACAATAATGTGATGTTTC 241
OY	293	cacatgttcaaccgtaaccgactatacgcgtgatgtatatctcgaagatggttttgtcacc 352
DB	242	CCCACGTACCCCGTACTGACTACACAGCTGATGTGATATCTCGAGGATGATTTTGTGACTC 301
OY	353	tctctactgaayaagtggaaaccaacgaagatgaacctcaagcttccccacgatgaaaatctgc 412
DB	302	TGCTAAGCTGAANAATGTTATACCAAGAGATGACCTTAGACTTCCAAACGATGAATGCTGTC 361
OY	413	tgaagcaaggttaaagaatyggtgtccagaaggaagaaagatcttgytgcgtttaatgtc 472
DB	362	TCTCCACATCATCAAGATGGATTTGGATGGAGATGAAAAGATTTGGTGTACAGATGATGCTT 421
OY	473	cgatggcggaagagagagattaacgccgctaagagatgttggtcaccaaga 521
DB	422	CATATGGGGAGAGCAGATTTGTGCTCTCAAGAGATTTGGCCCCAAGTA 470
RESULT 14		
LOCUS	AB004826	688 bp mRNA linear PLN 05-FEB-1999
DEFINITION	Solanum tuberosum mRNA for eukaryotic initiation factor 5A5, complete cds.	
ACCESSION	AB004826	
VERSION	AB004826.1 GI:2225884	
KEYWORDS	eukaryotic initiation factor 5A5. Solanum tuberosum (cultivar:Irish Cobbler) developing microtuber microtuber cDNA to mRNA. Solanum tuberosum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids I; Solanales; Solanaceae; Solanum.	
SOURCE	In J.G.	
ORGANISM	Direct Submission	
REFERENCE	Submitted (13-JUN-1997) Jun Gyo In, Hokkaido University, Faculty of Agriculture, Department of Botany, Kita 9 Nishi 9, Kita-ku, Sapporo, Hokkaido 060, Japan (E-mail:In@ez.hlines.hokudai.ac.jp, Tel:+81-11-706-2482, Fax:+81-11-706-2471) 2 (sites)	
AUTHORS	In,J.G., Fujino,K. and Kikuta,Y.	
TITLE	Nucleotide sequence of five cDNAs (Accession Nos. AB004823-AB004827) encoding eukaryotic translation initiation factor 5A (eIF-5A) from potato (PGR97-147)	
JOURNAL	Plant Physiol. 115, 864 (1997)	

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gene		64..543	
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CDS		64..543	
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BASE COUNT		181 a	137 c 161 g 209 t
ORIGIN			
Query Match		40.2%; Score 313.8; DB 8; Length 688;	
Best Local Similarity		77.9%; Pred. No. 1.2e-67;	
Matches 378; Conservative 0; Mismatches 107; Indels 0; Gaps 0;			
Oy	37	agaagcatgtcgcgcgaagaacacccatttggatcaaaagcagaatgctgcctcaaaa	96
Db	58	AAACGATGTGCGAGAGAGACACACTTGAAATCCAAAGCCAGCGGAGCTTCAAG	117
Oy	97	acttccacagcaagctggaacatccgtaagaatgctatcgttacaagccgt	156
Db	118	ACGTAACCTCAACAGCTGTGATCTGTAAGAGTGTGCATCGCATCAAAAATCG	177
Oy	157	ccctgcaaggttgcgtgcctccacttcaaaactggaacaacaggaatgctcaaat	216
Db	178	CCTTGCAGGAGGTGGAAGTTTGCACCTTCCACAGCAGCAGCAGCGTCAATATG	237
Oy	217	caacttctggaattgacatttcaatggaagaagaactggaagaatatcgtccgtcc	276
Db	238	CACCTTGTGSCAATTCACATTTTCTACTGGAAGAGCTTGAAGATATGTTCCCTCT	297
Oy	277	cacaatgtgctgcgcacatgttaacgtaacgtaacatagctgatactctctgaa	336
Db	298	CACAATGTGATGTCTCCATGTGAATGAGACGTGATATGAGCTTATGATCTGTGAG	357
Oy	337	gatggttctgtctcaacttctactgaaagtggaaacacgaagatgacctcaagctcc	396
Db	358	GATGCTTTGTGACTTTGTGACTGAAATGCTMAACACCAAGATGACTTGAGGCTCCCA	417
Oy	397	accgataaatactgctggaagcaggttaagaatggttccagaagaagaagaatctgtg	456
Db	418	ACTGATGATCTCTTCTTGCGCTCAAGTCAAAAGATGTTTTCGCGAGGGAAGACCTGG	477
Oy	457	gtctcttctatgctgcgtgagcgaagcagaatlaacgcgtttaaagctgtctgac	516
Db	478	CTGACAGGATGTCTGCCATGGAGAGAGACGATTTGTGTATCAAGACATTTGGCCCT	537
Oy	517	aagaa 521	
Db	538	AAGTA 542	
RESULT 15			
AF296081		810 bp	mRNA linear PLN 14-MAY-2001
LOCUS			
DEFINITION		Dianthus caryophyllus eukaryotic translation initiation factor 5A	
ACCESSION		AF296081	
VERSION		AF296081.1 GI:12407782	
KEYWORDS		clove pink.	
SOURCE		Dianthus caryophyllus	

REFERENCE		Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta: eudicotyledons: core eudicots; Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.	
AUTHORS		Wang, T.-W., Lu, L., Wang, D. and Thompson, J. E.	
TITLE		Isolation and Characterization of Senescence-Induced cDNAs Encoding Deoxyhypusine Synthase and Eukaryotic Translation Initiation Factor 5A from Tomato	
JOURNAL		J. Biol. Chem. 276 (20), 17541-17549 (2001)	
PUBMED		11278418	
REFERENCE		2 (bases 1 to 810)	
AUTHORS		Wang, T.-W., Wang, D., Lu, L. and Thompson, J. E.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-AUG-2000) Biology, University of Waterloo, Waterloo, ON N2L 3G1, Canada	
FEATURES		Location/Qualifiers	
source		1..810	
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BASE COUNT		232 a	152 c 192 g 234 t
ORIGIN			
Query Match		39.7%; Score 309.8; DB 8; Length 810;	
Best Local Similarity		76.5%; Pred. No. 1.2e-66;	
Matches 380; Conservative 0; Mismatches 117; Indels 0; Gaps 0;			
Oy	29	ctagaagaagacatgtgcgcgaagaacacacatttggatcaaaagcagaatgctggtg	88
Db	53	CGAAATGAGAGATGTGCGAGCAGATCACATTTGAGATCGCGCGCGGAG	112
Oy	89	cctcaaaaacttcccaagcagctggaacacatccgtaagaatggttatactgtatca	148
Db	113	CATCCAAGACTTACCCTCAACAGCTGTGATCAATCCGAGAGCGGTACATCGCATCA	172
Oy	149	aagcgctcccgcaaggttgttgaagctccacttcaaaaacttgaaaaacaggaacatg	208
Db	173	AAATGCGCCCTTGCAAGGTGTGAGGTTTCTACTCCAGACTGCAAGCGGTCAATG	232
Oy	209	ctaaatgtcaacttctggaattgacatttcaatggaagaagaactggaagaatctgttc	268
Db	233	CCAAATGTACTTTGTGCGATTCATTCACAGCGCAAGAGTGGAAAGATATTGTCC	292
Oy	269	cgctccccaacaattgtgctgacacatgttaacccgtaacgactacatgactgtatgta	328
Db	293	CCTCATCCCAATTTGTGTTCACATGTCACCGGTGCTCAACACGCTTGATTA	352
Oy	329	tctctgaagaatggttctgtctcaacttctactgtaagtggaacaacgaagatgacctca	388
Db	353	TCACGTGAAGATGCTTTGTGATCTGCTGACAGACAGTGTGACACCAAGATGATCTGA	412
Oy	389	ggcttcccaacgtgaanaactgtctgaagcaggttaagaatggttccagaagaagaag	448
Db	413	AGCTTCCTGCTGATGAGGCCCTTGTGAAGACAGATGAAGAGGATTTGAGCGGGAAG	472
Oy	449	acctgtggtctgtcttgaatgctgcgtgagcgaagcagaatcaacgcgttaagatg	508
Db	473	ACTTGATCTGTGACGATGATGCAATGTGCAATGTGAGAGACGACATTCGCCGCTCAAGACG	532
Oy	509	tctgtaacgaatgag 525	
Db	533	TTAGTGTGTGCAAGTAG 549	

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